SEQUENCE LISTING

<110> JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA

<120> COMPOSITIONS AND METHODS RELATING TO
    HYPERTENSION

<130> 22000.0110U2

<150> 60/228,947
<151> 2000-08-29

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
    synthetic construct

<221> misc_feature
<222> (1)...(4123)
<223> n = g, a, c or t(u)

<400> 1
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ttgtaaaatg accacaaagt gggctaaaag ttcagacgta tggagcatgt ccctctcggt   180
ctttggtttt gaccaaagct cagaattgtg gaaagaaaga aaaagtagtg ggttatgcat   240
gttgtgtcac agtggaagat gaagtagtgg gtgttaaaga aaatgtttgg atagataaag   300
gatcaagtga gcggcaaaca cacattcctg gcagagtgaa tgggctggct ttctagagat   360
tcttgttaaa ataccttttg tgtttgcctc tttgtggtct tcacaactag gattaattta   420
gggaagataa tcatgatcca ggtgaggata aagattccag agaaaggctt atttctaccc   480
cttaacttct ttgttttttct tcctttctaa aagtttttgtc attttttaaaa tttatttttt   540
atttaatttt tttcatgcaa tataatttga tcatattctt tccttcctcc aacttctcct   600
agatcctcag ggccttccta gctatccatc ttcatgttaa tggatagact gacaaccaaa   660
acattctttc tctgcttaaa taatatctcc ataaaatcta taaataaatg aggtagttgg   720
aaactatctc agcactttttc aattgattgg ctagtaatcc ttcaatatct cattttttttt   780
aactttcgct ttatctattc tgtgtgnaca ttaattttttt tcaggcaagg cataatatat   840
atataattgg actgatttct ttattagagt ttgccctatg tgaggtcaag aaatattctt   900
aaattaatga gtgactgaat aagtgatggg caatttaagt atttagaaaa gaaaggtttt   960
attattccat tcagtcaaga tagtgagaca gagaaagagt ctgtcacagg ctgtgtatgt  1020
ggtgaggctg attgagtctt gagccacctg aatgcaactg cactgttcca cctgctggca  1080
catccatcct ggatcaatct ggagtgtgac tgtgacaagt ctcagataaa atggaagaaa  1140
cagctggatt tggagtccag atgcaaagat gactataggt agaaactttc agcaattaca  1200
ttcatctgaa cacaccaact actgttgtca tcatttcacc ctgaaattag gaaaatagta  1260
caagcagcta cacctattac atgtttggta aattagaatg tgaatttctt aatatccagg  1320
ttaatgtcta gtccatgact ttacctcatc agcaaggata tacataacat gcaatatgtg  1380
ctcataaat agttgtgagt agttcagaga aatgggaatt ggtatacata tagatgttac  1440
caagactaga tactagagat ttgtttttac tgtttaccaa agctgatgtt gcagattaat  1500
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gtgtgtctac cttctcatga cttaaatgcg ggtttctaaa catttagtga cactagtgat  1620
ccagaaacta ctaaccatgg gttttttttt atttagccct acaaggtact tggatggtat  1680
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ctctgggttc ttccaatggg ccttcttgct cagtctattt ctggtgctgt tcaaggcagt    1740
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ttcccactgg ctttgggggc accatctgaa gggacaagga gctccagcag attcttatat    1860
gggtagagaa attcccaagt gcctgcttac agtgtctctc ggggagcaat atacgagtcc    1920
tgctttatga tcctgactat gtgaaggtgg ttctggggag atcagatcca aaggcttctg    1980
gaatttatca attctttgct ccctggattg gttatggttt gctcctgttg aatgggaaga    2040
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atgtcaaaat catggcggac tctgtcaata taatgctaga taaatgggag aagcttgatg    2160
gccaggacca ccctctggag atcttccact gtgtttcatt gatgacactg gacactgtta    2220
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ccagaatgga ggataggaac agcttgtctg atgaggacct gcgtgcagag gtggacacat    2580
tcatgtttga gggtcatgac actacagcca gtggaatttc ctggattttc tatgctctgg    2640
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tacatcataa cccacgtttc tggccaaacc caaaggtgtt tgacccctct agatttgcac    2940
cagattcttc tcaccatagc catgcttatc tgccattctc aggaggatca aggaactgca    3000
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ccaagaatgg gatccacctg tgtctcaaga agctaagata attctgatgg agtcagggca    3180
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ttcacccctc ataaccattg cactgacaga ggaagatata ttttagaggg agacacttgt    3480
acctttctct cccttcagtt attagactct tgggacaatg gacatcatga attaaaacgt    3540
tcttagaaat cacatgctgg gagaaaatta acactaaaat ctggtaccag ccagaggaag    3600
gaacttgact caaaataaga gattttttaga tatttctgtc tgtctcatag ttaaaattaa    3660
tgttttcctg ctttctggca tatgcctcat cttttctatg aagtagtaat actgatacag    3720
aaaggtagag agaaatgaat agtttttgct actttgggcc aaactgtgaa aaaatccatt    3780
ttatttcatc aatttctgtt tcccaatttc atttaagaca caggaaaact actcagcatg    3840
aactttgggg agccagagca gttttggcaa tccaggggaag catgttgcca tctggtccct    3900
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gagctggttg tgtagaaatg caggttggcg tttttttgtga agctaaggag ttttctgact    4020
ttaacccggt cttatttgtt tagagtactc tgattattca ctttagtgat ttggagaatt    4080
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```

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<210> 2
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 2
Met Gly Phe Phe Val Phe Ser Pro Thr Arg Tyr Leu Asp Gly Ile Ser
1               5                   10                  15
Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
            20                  25                  30
Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
        35                  40                  45
```

```
Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
    50                  55                  60
Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
65                  70                  75                  80
Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
                85                  90                  95
Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
            100                 105                 110
Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
        115                 120                 125
Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
    130                 135                 140
Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
145                 150                 155                 160
Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
                165                 170                 175
Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
            180                 185                 190
Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
        195                 200                 205
Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
    210                 215                 220
Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
225                 230                 235                 240
Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
                245                 250                 255
His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
            260                 265                 270
Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
        275                 280                 285
Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
    290                 295                 300
Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
305                 310                 315                 320
Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
                325                 330                 335
His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu
            340                 345                 350
Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
        355                 360                 365
Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
    370                 375                 380
Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
385                 390                 395                 400
Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
                405                 410                 415
His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
            420                 425                 430
Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
        435                 440                 445
Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
    450                 455                 460
Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
465                 470                 475                 480
Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
                485                 490                 495
Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
            500                 505
```

4

<210> 3
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
     synthetic construct

<400> 3
Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
1   5   10   15
Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Leu Phe
            20   25   30
Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
        35   40   45
Gln Gln Phe Pro Ser Pro Pro Ser His Trp Leu Phe Gly His Lys Ile
    50   55   60
Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
65   70   75   80
Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
                85   90   95
Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
            100   105   110
Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
        115   120   125
Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
    130   135   140
Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
145   150   155   160
Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
            165   170   175
Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
            180   185   190
Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
        195   200   205
Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
    210   215   220
Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
225   230   235   240
Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
            245   250   255
Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
        260   265   270
Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Lys Arg Arg Leu Asp
    275   280   285
Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
    290   295   300
Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
305   310   315   320
His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
            325   330   335
Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
            340   345   350
Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
        355   360   365
Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
    370   375   380

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Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
385                 390                 395                 400
Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
                405                 410                 415
His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
                420                 425                 430
Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
            435                 440                 445
Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
        450                 455                 460
Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
465                 470                 475                 480
Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
                485                 490                 495
Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
            500                 505
```

<210> 4
<211> 2116
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 4
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caaagaggct gttcaggtcc atcaaccctg gtcttgaaat caagctctgc tcacacccct        180
ctccctcccc caagtaggtg gggcaacctc cctggggttt gcagacagga gggtgttcat        240
tgaaagtgaa ggagagttgg tgatccagaa gctgttgtat catgagtgcc tctgctctga        300
gctccatcag attcccagga agcatctctg agtaccttca agtagcctct gtgctcagcc        360
tgctcctgct gctcttcaag acagcccagc tctacctgca caggcaatgg ctactcagca        420
gtactcagca gttcccatcc ccaccttctc actggctctt tggacacaag atcttaaagg        480
accaggacct tcaagatatt ctaactagga ttaagaattt cccaagtgcc tgtccacagt        540
ggctctgggg aagcaaagtg cgcattcaag tgtatgaccc tgactacatg aagctgattc        600
tggggagatc agaccaaaa gctaatggtt cctacagatt tctagctccc tggattgggc        660
gtggtttgct tatgctggat ggacagacat ggtttcagca ccgacgaatg ttgaccccag        720
ctttccacta tgacattctg aagccttata cggaaatcat ggcagactct gttcgtgtaa        780
tgctggataa atggaacag attgttggcc aggattccac cctggagatc tttcgacaca        840
tcaccttgat gaccttggac accatcatga agtgtgcctt cagccacgag ggcagtgtcc        900
agttggacag aaaatacaag tcctatatcc aggcagttga ggacctgaac gatctcgttt        960
tttcccgtgt gcggaacatc tttcacctga atgacatcat ctacagagtg tcctctaatg       1020
gctgcaaggc taacagtgcc tgcaaacttg cccatgatca cacagaccaa gtgatcaaat       1080
caaggaggat tcaacttcag gatgaggaag agttggaaaa gcttaagaag aaaaggcgat       1140
tggatttcct ggacatcctc ctatttgcca gaatggaaaa tggaaaaagc ttatctgata       1200
aggaccttcg tgctgaagtg gatactttca tgttcgaggg ccatgacacc acagctagtg       1260
gtatctcctg gatcttctat gctttggcca caaatcctga acatcaacag agatgcagga       1320
aggagatcca aagtctccta ggagatggga cttctatcac ctggaatgac ctggacaaga       1380
tgccctatac taccatgtgc atcaaggagg ccctgaggat ctaccctcct gtaccaagtg       1440
tgagcagaga gctcagctca cctgtcacct ttccagatgg acgttcttta cccaaaggta       1500
tccatgttat gctctccttt tatggccttc atcacaaccc aactgtgtgg ccaaatccag       1560
aggtgtttga tccttctcga tttgcaccag ggtcttcccg gcacagccac tcattcctgc       1620
ccttctcagg aggagcaagg aactgcattg ggaaacagtt tgcgatgaat gagctgaagg       1680
tggctgtggc cctgaccctg ctccgctttg agctgctgcc agatcccacc agagtcccaa       1740
tccccatacc aagaattgtg ttgaagtcca agaatgggat ccacttgcat ctcaaagagc       1800
tccaataatc ttcacaggac aagacagctc aaatgcatgc tgcctgccat tctgtctttc       1860
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tgtcacttac tctttttcccc aatccttctg ctcacatctc attctttctt ctcaccttgt      1920
tcacctccac ccaccttctg ctgggcttcc agtctccttg cctgtcagtc tttttcaact      1980
tcttctgaga tccctacttg cttttctctc tacctgtccc taaccagact gcatgtttga      2040
cctttgactt taatgatctc cctaacttgc accctgcctt tcttttctgt gtatttcctt      2100
ctcttctact cttgtc                                                      2116
```

<210> 5
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 5

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Met Ser Val Ser Val Leu Ser Pro Ser Arg Leu Leu Gly Asp Val Ser
1               5                   10                  15
Gly Ile Leu Gln Ala Ala Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Val Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Leu Gln Gln Asp Gln Glu Leu Gln Arg Ile Gln Lys Trp Val Glu
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro His Trp Leu Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
                100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
                180                 185                 190
Thr Leu Asp Thr Ile Met Lys Cys Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
    210                 215                 220
Asn Asn Leu Val Phe Ser Arg Val Arg Asn Ala Phe His Gln Asn Asp
225                 230                 235                 240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                 250                 255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
                260                 265                 270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
        275                 280                 285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
    290                 295                 300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                 310                 315                 320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                 330                 335
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Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
            340                 345                 350
Ser Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
        355                 360                 365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
    370                 375                 380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                 390                 395                 400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                405                 410                 415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Pro Glu Val Phe Asp
                420                 425                 430
Pro Phe Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
        435                 440                 445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
    450                 455                 460
Asn Glu Leu Lys Val Ala Thr Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                 470                 475                 480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                485                 490                 495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
                500                 505                 510
Cys Glu Asp Lys Asp Gln Leu
            515


<210> 6
<211> 2576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
        synthetic construct

<400> 6
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tgctgatcaa ggcagttcag ctctacctgc acaggcagtg gctgctcaaa gccctccagc        180
agttcccgtg ccctccctcc cactggctct tcgggcacat ccaggagctc aacaggacc         240
aggagctaca acggattcag aaatgggtgg agacattccc aagtgcctgt cctcattggc        300
tatgggggag caaagttcgt gtccagctct atgaccctga ctatatgaag gtgattctgg        360
ggagatcaga cccgaaatcc catggttcct acagattcct ggctccatgg attgggtacg        420
gcttgctcct gttgaatggg cagacatggt tccagcatcg acggatgctg accccagcct        480
tccactatga catcctgaag ccctatgtgg ggctcatggc agactctgta cgagtgatgc        540
tggacaaatg ggaagagctc cttggccagg attccccctct ggaggtcttt cagcacgtct        600
ccttgatgac cctggacacc atcatgaagt gtgccttcag ccatcagggc agcatccagg        660
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cccgtgtgag gaatgccttt caccagaatg acaccatcta cagcctgacc tctgctggcc        780
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ggaaggctca actacagaag gagggggagc tggagaagat caagaggaag aggcatttgg        900
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acctccgtgc tgaggtggac acgttcatgt ttgagggcca cgacaccaca gccagtggga       1020
tctcctggat cctctatgct ctggccacac accccaagca tcaggagagg tgccggggagg       1080
agatccacag cctcctgggt gatggagcct ccatcacctg gaaccacctg gaccagatgc       1140
cctacaccac catgtgcatt aaggaggcac tgaggctcta cccaccggtg ccaggcattg       1200
gcagagagct cagcactccc gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca       1260
tggtcctcct ctccatttat ggccttcacc acaacccaaa agtgtggccc aacccagagg       1320
tgtttgaccc tttccgtttt gcaccgggtt ctgctcaaca cagccacgct ttcctgccct       1380
```

8

```
tctcaggagg atcaaggaac tgcattggga aacaatttgc catgaacgag ctgaaggtgg    1440
ccacggccct gaccctgctc cgctttgagc tgctgcctga tcccaccagg atccccatcc    1500
ccattgcacg acttgtgttg aaatccaaaa atggaatcca cctgcgtctc aggaggctcc    1560
ctaacccttg tgaagacaag gaccagcttt gagggcctcc acctgccgtc ctgtcttcct    1620
gaccccgct tctgtcccct tcctgtctgc ccatatcctg ttttctgtct gcccaccttc    1680
ccttcttccc acctgcctgc tgtcccccag tctgcctgcc cttctctctc tcacctttct    1740
ccaggctccc tacctgcttg tctacctgtc tcctacccac ctgtatctct tgttgggaga    1800
aaagctgagt gttgggagaa gctgaggccg agcttgcatg tctgacataa tgtaaaagag    1860
tcttgaatca tgtccaggat ccagggtcta aaaccccttg tggcctttgg aacaccaagc    1920
tctgtgctga agggtggaag gctaccctga cgcaccataa tctaagcccg gggcataaaa    1980
cccctcgtgg cttggataga atccagggct cgtggctctg gaatgtgtct ggacttgctg    2040
gctccttgct ccttgctctc ccaggatcaa ttgtatcttg agttaaaaga acctgctctc    2100
cattatctca agtaacagag cagatgctaa accgtcacag ctgtaaattg tgtgcttaat    2160
gcaacatgcc ctttcgaccc accccccatt ctcaccacct gtttctttgt ttgatcacca    2220
ataaataatc tgcacttcca gagctcgggg ccttcacagc ctccatcctt agctttggcg    2280
ccctggaccc actttctctc tcaaactgtc ttttctcact gctttgactc tgccggactt    2340
tgtcacccccc acgacctggt gttgggtctg aacacccaa catccctgaa tctccaccca    2400
cctcccaaac tcctgcctgc cctccagact gtctgcccat acacctgtct ccttcttcct    2460
gcctggcttg tctgttccta tattagtttc ctattactgc tgtaataaac tatcacaatc    2520
tcagtgattt taaataaaaa aaaaaaaaaa aaaaaaaaa aaaaaaaacg gaattc         2576
```

<210> 7
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 7
```
Met Ser Val Ser Val Leu Ser Pro Ser Arg Arg Leu Gly Gly Val Ser
1               5                   10                  15
Gly Ile Leu Gln Val Thr Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Phe Gln His Asp Gln Glu Leu Gln Arg Ile Gln Glu Arg Val Lys
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro Tyr Trp Ile Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
                100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Arg Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Asn Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
                180                 185                 190
Thr Leu Asp Thr Ile Met Lys Ser Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
```

```
       210                   215                   220
Asn Ser Leu Val Phe Cys Cys Met Arg Asn Ala Phe His Glu Asn Asp
225                   230                   235                   240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                  245                   250                   255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
              260                   265                   270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
          275                   280                   285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
      290                   295                   300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                   310                   315                   320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                  325                   330                   335
Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
              340                   345                   350
Gly Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
          355                   360                   365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
      370                   375                   380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                   390                   395                   400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                  405                   410                   415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Leu Glu Val Phe Asp
              420                   425                   430
Pro Ser Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
          435                   440                   445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
      450                   455                   460
Asn Gln Leu Lys Val Ala Arg Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                   470                   475                   480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                  485                   490                   495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
              500                   505                   510
Cys Glu Asp Lys Asp Gln Leu
          515
```

<210> 8
<211> 1872
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 8

```
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aatgctcatt aaatatttgt gaggtacatg gacaggggaa tgtggtagac agctgatgaa     120
gctgttctcc cactgttccc ctaggtggat catccaaagt caatcgattc tgaactctga     180
ggtccaagtt ctgccctccc ccttcactct ccccacaagt gggcgggaca atcctcccat     240
gacttaagca caggtggaca ggggtggtca gagagaggaa ggggcactca gagatccagc     300
aggtgctgca ccatgagtgt ctctgtcctg agcccagca gacgcctggg tggtgtctcc      360
gggatcctcc aagtgacctc cctgctcatt ctgcttctgc tgctgatcaa ggcagctcag     420
ctctacctgc ataggcagtg gctgctcaaa gccctccagc agttcccgtg ccctccctcc     480
```

```
cactggctct tcgggcacat ccaggagttc caacacgacc aggagctaca acggattcag     540
gaacgggtga agacattccc aagtgcctgt ccttattgga tatggggagg caaagttcgt     600
gtccagctct atgaccctga ctatatgaag gtgattctgg ggagatcaga cccgaaatcc     660
catggttcct acagattcct ggctccacgg attgggtacg gcttgctcct gttgaatggg     720
cagacatggt tccagcatcg acggatgctg accccagcct tccacaatga catcctgaag     780
ccatatgtgg ggctcatggc agactctgta cgagtgatgc tggacaaatg ggaagagctc     840
cttggccagg attcccctct ggaggtcttt cagcacgtct ccttgatgac cctggacacc     900
atcatgaaga gtgccttcag ccatcagggc agcatccagg tggacaggaa ttctcagtcc     960
tacatccagg ccattagtga cctgaacagc ctggtttttt gctgtatgag gaatgccttt    1020
catgagaatg acaccatcta cagcctgacc tctgctggcc gctggacaca ccgcgcctgc    1080
cagctggccc atcagcacac agaccaagtg atccaactga ggaaggctca actacagaag    1140
gaggggggagc tggagaagat caagaggaag aggcacttgg attttctgga catcctcctc    1200
ttggccaaaa tggagaatgg gagcatcttg tcagacaagg acctccgtgc tgaggtggac    1260
acgttcatgt ttgagggcca cgacaccaca gccagtggga tctcctggat cctctatgct    1320
ctggccacac accccaagca tcaggagagg tgccgggagg agatccatgg cctcctgggt    1380
gatggagcct ccatcacctg gaaccacctg gaccagatgc cctacaccac catgtgcatt    1440
aaggaggcac tgaggctcta cccaccggtg ccaggcattg gaagagagct cagcactccc    1500
gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca tggtcctcct ctccatttat    1560
ggccttcacc acaacccaaa agtgtggccc aacctagagg tgtttgaccc ttcccgtttt    1620
gcaccgggtt ctgctcaaca cagccacgct ttcctgccct tctcaggagg atcaaggaac    1680
tgcatcggga aacaatttgc catgaaccag ctgaaggtgg ccagggccct gaccctgctc    1740
cgctttgagc tgctgcctga tcccaccagg atccccatcc ccattgcacg acttgtgttg    1800
aaatccaaaa atggaatcca cctgcgtctc aggaggctcc ctaacccttg tgaagacaag    1860
gaccagcttt ga                                                        1872
```

<210> 9
<211> 21990
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> misc_feature
<222> (1)...(21990)
<223> n = g, a, c or t(u)

<400> 9
```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1080
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1140
```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1200
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1260
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1320
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1380
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1440
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1560
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1620
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2160
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2460
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnggt    2520
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tgagccccag cagactcctg ggtgatgtct ctggaatcct ccaagcggcc tccctgctca    2640
ttctgcttct gctgctgatc aaggcagttc agctctacct gcacaggcag tggctgctca    2700
aagccctcca gcagttcccg tgccctccct cccactggct cttcgggcac atccaggagn    2760
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2820
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    4620
```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   4680
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   4740
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ggcaaagttc gtgtccagct ctatgaccct gactatatga aggtgattct ggggagatca   6000
ggtgagatcg aacccccatc ccaactgcaa tttctcttcc ctcttgacac atgcccctgg   6060
gtctgtaaaa ttccagaaga gagtggctgt tcaaacatca atatctgaaa cctctcccac   6120
gcatccacca agcccaccat gcccaggctg tagtcaaaaa tatttatgaa tactgaatgt   6180
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ttaaattttc tgaaacgtaa attgccccag atctgtaaaa caaatttcat acccacattg   6300
acttgggttc gaagctctaa ttgttgcctg tcctggtcag gaggtgacta ggaaaacatc   6360
aatgtagaaa aacccatggc tctgtattat tcattgtcat tgaagaccta gcctatgtat   6420
ctcaccaatt caccttccta gcccctgggt gttttcctgc tggaacactg agtctgtctt   6480
cctgagccca cattgacctt caggacagaa atagaagtgg atgggagtca agtgggaggt   6540
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ttcttagtaa ctcctagttt cctataaagc cctttcttgc ctttcagacc cgaaatccca   6660
tggttcctac agattcctgg ctccatggat tggtatgtgt gcaaactagg actgcagccc   6720
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ccactatcat gacctcatcc ccaaatcaag cctcacttcc ttcttctaac aagaccctca   6840
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gttctctcca gacatccttg gcttcacatt tattttacat ctgcccacaa cccttttcaa   6960
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cagccnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn cctgacacac acacacac    7200
acacaaacac acattcatgt ctctcttagg gtacggcttg ctcctgttga atgggcagac   7260
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnaaaccc tgtgtcccac   7440
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20160
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20520
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20580
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20640
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20700
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20760
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20820
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20880
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20940
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21060
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21180
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21540
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21660
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21840
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn                                    21990
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